



# **STIC Search Report**

## **Biotech-Chem Library**

STIC Database Tracking Number 114903

**TO: Ruixiang Li**  
**Location: REM-4D75**  
**Art Unit: 1646**  
**Thursday, February 26, 2004**

**Case Serial Number: 09742684**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**Remsen 1A59**  
**Phone: 571-272-2523**

**toby.port@uspto.gov**

### **Search Notes**

Dear Examiner Li,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port

Thu Feb 26 13:51:32 2004

US-09-742-684a-15.rmpb

Page 1

GenCore version 5.1.6  
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ON nucleic - nucleic search, using SW model

Run on: February 26, 2004, 02:42:01 / Search time 3:01 Seconds  
(without alignments)

Title: US-09-742-684a-15

Prefix: 1 cctcagagagacccagcggga.....accgccttcacacagac 2563

Sequence: 1 cctcagagagacccagcggga.....accgccttcacacagac 2563

Scoring table: INSTRUTY NNC  
Gapop 10.0 / Repeat 1.0

Searched: 235733 seqs, 160733377 residues 4707466

Total number of hits satisfying search parameters:

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 48 similarities

Database: Published Applications RN\* /US07 PIRNCMB.seq\*

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Result No. Score Match Length DB ID Description  
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# ALIGNMENTS

RESULT 1: US-09-742-684-1  
GENERAL INFORMATION:  
Parent No. US001003036ML  
APPLICANT: Mathias Lawrence S.  
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
NUMBER OF SEQUENCES: SEVENTY (5) OF THE ACTIVE/TOX-BETA SUPERFAMILY  
CORRESPONDENCE ADDRESS:  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90013  
COMMENTS:  
MEDIUM TYPE: Plasmid  
COMMENTS: IBM PC compatible  
SEQUENCE: Plasmid Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/742,684  
CLASSIFICATION:   
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/476,133  
PRIORITY DATE: 02-SEP-1994  
APPLICATION NUMBER: US 08/700,584  
PRIORITY DATE: 02-SEP-1994  
APPLICATION NUMBER: US 07/773,229  
PRIORITY DATE: 03-OCT-1991  
APPLICATION NUMBER: US 07/699,709  
PRIORITY DATE: 10-JAN-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen S.  
REGISTRATION NUMBER: 31,192  
EXPIRATION DATE: 01/01/2005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-566-4737  
FACSIMILE: 619-566-9392  
INFORMATION: 619-566-9392  
LENGTH: 2563 base pairs  
SEQUENCE CHARACTERISTICS:  
TYPE: nucleic acid  
SOURCE: human  
TOPOLOGY: linear  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 71..1609  
SEQUENCE DESCRIPTION: SEQ ID NO: 1  
US-09-742-684-1

Query Match 99.7%; Score 2556.4; DB 9; Length 2563;  
Best Local Similarity 99.8%; Freq. No. 0;  
Matches 2557; Conservative 21; Mismatches 41; Indels 0; Gaps 0;

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DB 1801 CAGATTTGAGAGAGATTTGAGAGATTTGATGAGAGATTAAGCTGTGTAAATGTG 1860







Vale, Wylie M.  
Molecular Cloning AND Recombinant Production OF  
TITLE OF INVENTION: RECEPTOR(S) OF THE ALPHA7/GCF-BETA SUBFAMILY

NUMBER OF SCIENCES: 14  
COMBINED ADDRESS: Bretts Schroeder, Buengemann & Clark  
STREET: 444 South Plover Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071

COMPUTER READABLE FORM:  
OPERATING SYSTEM: IBM PC-DOS/MS-  
SOFTWARE: Patent In Release #1.0, Version #1.25  
APPLICATION NUMBER: US/09/742,684  
PILING DATE: 19-Dec-2000  
CLASSIFICATION: -Chemo-

PRIOR APPLICATION NUMBER: 08/476,133  
PILING DATE: Unknown  
APPLICATION NUMBER: US 08/500,584  
PILING DATE: 19-MAY-1992  
APPLICATION NUMBER: US 07/860,220  
PILING DATE: 08-MAY-1992  
APPLICATION NUMBER: US 07/773,226  
PILING DATE: 08-MAY-1992  
APPLICATION NUMBER: US 07/698,709  
PILING DATE: 10-MAY-1991

ATTORNEY/AGENT INFORMATION: E  
REGISTRATION NUMBER: 31,192  
REFERENCE /DOCKET NUMBER: PI 9927

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-9377  
TELEX: 619-546-9392

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS  
LENGTH: 1321  
TYPE: nucleic acid  
STANDARD: linear  
MOLECULAR WEIGHT: 468.1997  
IMMEDIATE SOURCE:  
FEATURES: NACFR  
FEATURES/KEY: CDS  
LOCATION: 468..1997

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

LS-05-742-684-3

Query Match      26.5% Score 778.2; D8 9; Length 235;  
Best Local Similarity    65.6%; Pied No. 6;le-169;  
Matches 1051; Connective   2; Mismatches 356; Indels 15; Gaps 3

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[illegible]







SULT 9 405-78  
 Sequence 78, Application US/10/08605  
 Publication No. US2002060934A1  
 GENERAL INFORMATION: Julie  
 APPLICANT: Stem, Lynn  
 APPLICANT: Bachmann, Jane  
 TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF  
 FILE REFERENCE: 311338 NUMBER: US/10/108,605  
 CURRENT FILING DATE: 2002-03-27  
 PRIOR APPLICATION NUMBER: US/97/61,142  
 PRIOR FILING DATE: 2001-01-16/01/76,418  
 PRIOR FILING DATE: 2000-01-14  
 NUMBER OF SEQ ID NOS: 361  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 8  
 LENGTH: 2887  
 TYPE: DNA  
 ORGANISM: Drosophila melanogaster  
 S-10-108-605-78  
 Query Match 12 44; Score 316.9; Db 13; Length 2687;  
 Best Local Similarity 60.94; Pct. Identities 35; Indels 12; Gaps 3;  
 Matches 570; Conservative 1; Mismatches 351;

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 y 979 TACCCGACGACGCTTACGATACAACTATCGATCTCTGACGACCGTCCATTC 1038  
 b 648 AGCTTTTGAAGTGAAGCAGGCGAGATTTGGTGTCTGGAAGGACGTTCTCT 707  
 b 1039 ACCTCTGACGACGACGCTCTGCTGATCTGATGATGATGATGATGATGATGAT 1098  
 y 708 ATGAATATGGCTCTCAAAATTTCTCAATGACGACGACGCTCTGCGAGATGAT 767  
 y 1099 ATCGAGATGGCTCTCAAAATTTCTCAATGACGACGACGCTCTGCGAGATGAT 1158  
 b 768 ATGAATATGGCTCTCAAAATTTCTCAATGACGACGACGCTCTGCGAGATGAT 827  
 b 1159 AGATATCTGACGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1218  
 y 828 AGAAGACGACGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 887  
 y 1219 AGA-----GCACTATGACGACGATATGCTGATATGCTGATATGCTGATATG 1272  
 y 888 GCTGATCTGATGATCTTGAAGCTATATGCTGATATGCTGATATGCTGATATG 947  
 y 1273 ATCTCTCTGATCTTGAAGCTATATGCTGATATGCTGATATGCTGATATGCTGAT 1332  
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 Qy 1425 CATCTCTGTCGACGACGCTCTGTCGACGACGCTCTGTCGACGACGCTCTGAT 1484  
 Db 1810 ATGATTTTTCGACGACGCTCTGTCGACGACGCTCTGTCGACGACGCTCTG 1869  
 Qy 1485 CTGAGATGTCGACGACGCTCTGTCGACGACGCTCTGTCGACGACGCTCTG 1520  
 Db 1870 CTCTGCTGATGACGACGCTCTGTCGACGACGCTCTGTCGACGACGCTCTG 1905  
 RESULT 10  
 US-09-918-995-30472  
 Sequence 30472, Application US/09/995  
 Publication No. US2003007623A1  
 GENERAL INFORMATION: Hyves, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM THE GENOME OF THE HOUSEFLY, MUSCA DOMESTICA L.  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918,995  
 CURRENT FILING DATE: 2001-07-26  
 PRIOR FILING DATE: US/09/215,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: PatSeq for Windows Version 3.0  
 SEQ ID NO: 30472  
 LENGTH: 535  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 NAME/KEY: misc feature  
 LOCATION: (1)...(535)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-30472  
 Query Match 9 34; Score 238.2; Db 10; Length 535;  
 Best Local Similarity 74.1; Pct. Identities 32; Indels 3; Gaps 1;  
 Matches 349; Conservative 1; Mismatches 129;

Qy 784 ACCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 843  
 Db 75 ACCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 134  
 Qy 844 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 903  
 Db 135 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 194  
 Qy 904 TTTTAAAGGCTATGCTCTCTGATGATGATGATGATGATGATGATGATGATG 963  
 Db 1395 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 254  
 Qy 964 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
 Db 255 AGGCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 314  
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 Db 315 TTTTCT 374















while genome was made by sequencing genomic exons and ordering

FEATURES

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/gene="ACVR2"
/locus_tag="H03073"

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sl. 21427

50.94; score 1303.4; DB 29; Length 1427;

Local similarity 94.0%; Pred. No. 0;

1398; Conservative 2; Mismatches 4; Indels 84; Gaps 1;

184

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[illegible]

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106 K S E C A G C A G C C N G C A G C C T T G C T A T G T G T A T A A G A T A A C G G C G A 244

[illegible]

94. AGGAGACAGAACCCACCAGACTGGTGTGAACTTGCCTATGGTGATAAAGATAACGGCGA 143

© 1998 by The American Psychological Association 0893-3200/98/0000-0000\$05.00/0

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147

144 CATT-----

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100

365 GAAGTGTACTTTGTTGCTGTGAGGGCAATATGTGTAAAGAAAGTTCTCTTAATTTCOG 424

The diagram illustrates the experimental design across two studies. Study 1 involves participants and stimuli leading to results. Study 2 involves participants and stimuli, where the stimuli are derived from the results of Study 1, leading to results.

180 GAAGTGTACCTTTTGTCTGTGAGGGCAATATGTGTATGAAAGTCTCTATTTCGG 239

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**Figure 1**

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419

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[illegible]



















GenCore version 5.1.6  
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1 nucleic - nucleic search, using sw model

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run on:      February 26, 2004, 00:06:40 / Search time 930 Seconds
              (without alignments)
              11707.668 Million cell updates

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US-09-742-684A-15

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effect score: 2563
sequence: 1 cccacgagagacccagga.....aacacgcttcacagatgcc 2563

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[illegible]

scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

attached: 3373863 secs. 2124099041 res: dies

[illegible]

total number of nice satisfying ch

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minimum DB seq length: 0
maximum DB seq length: 200000000

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not-processing. Minimum Match 02

Maximum Match 100%

usage :

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2: genseq1990b:
3: genseq2000a:
4: genseq2001a:
5: genseq2001b:
6: genseq2002a:
7: genseq2003a:
8: genseq2003b:
9: genseq2003c:
10: genseq2004a:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Unit No	Score	%	Length	DB	ID	Description
1	2661	99.9	2563	2	AAK22685	Human act
2	2662	99.9	2563	2	AAK22685	Human act
3	2663	99.9	2563	2	AAK22685	Human act
4	2664	99.9	2563	2	AAK22685	Human act
5	2665	99.9	2563	2	AAK22685	Human act
6	2666	99.9	2563	2	AAK22685	Human act
7	2667	99.9	2563	2	AAK22685	Human act
8	2668	99.9	2563	2	AAK22685	Human act
9	2669	99.9	2563	2	AAK22685	Human act
10	2670	99.9	2563	2	AAK22685	Human act
11	2671	99.9	2563	2	AAK22685	Human act
12	2672	99.9	2563	2	AAK22685	Human act
13	2673	99.9	2563	2	AAK22685	Human act
14	2674	99.9	2563	2	AAK22685	Human act
15	2675	99.9	2563	2	AAK22685	Human act
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20	2680	99.9	2563	2	AAK22685	Human act
21	2681	99.9	2563	2	AAK22685	Human act
22	2682	99.9	2563	2	AAK22685	Human act
23	2683	99.9	2563	2	AAK22685	Human act
24	2684	99.9	2563	2	AAK22685	Human act
25	2685	99.9	2563	2	AAK22685	Human act
26	2686	99.9	2563	2	AAK22685	Human act
27	2687	99.9	2563	2	AAK22685	Human act
28	2688	99.9	2563	2	AAK22685	Human act
29	2689	99.9	2563	2	AAK22685	Human act
30	2690	99.9	2563	2	AAK22685	Human act
31	2691	99.9	2563	2	AAK22685	Human act
32	2692	99.9	2563	2	AAK22685	Human act
33	2693	99.9	2563	2	AAK22685	Human act
34	2694	99.9	2563	2	AAK22685	Human act
35	2695	99.9	2563	2	AAK22685	Human act
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37	2697	99.9	2563	2	AAK22685	Human act
38	2698	99.9	2563	2	AAK22685	Human act
39	2699	99.9	2563	2	AAK22685	Human act
40	2700	99.9	2563	2	AAK22685	Human act
41	2701	99.9	2563	2	AAK22685	Human act
42	2702	99.9	2563	2	AAK22685	Human act
43	2703	99.9	2563	2	AAK22685	Human act
44	2704	99.9	2563	2	AAK22685	Human act
45	2705	99.9	2563	2	AAK22685	Human act
46	2706	99.9	2563	2	AAK22685	Human act
47	2707	99.9	2563	2	AAK22685	Human act
48	2708	99.9	2563	2	AAK22685	Human act
49	2709	99.9	2563	2	AAK22685	Human act
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52	2712	99.9	2563	2	AAK22685	Human act
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54	2714	99.9	2563	2	AAK22685	Human act
55	2715	99.9	2563	2	AAK22685	Human act
56	2716	99.9	2563	2	AAK22685	Human act
57	2717	99.9	2563	2	AAK22685	Human act
58	2718	99.9	2563	2	AAK22685	Human act
59	2719	99.9	2563	2	AAK22685	Human act
60	2720	99.9	2563	2	AAK22685	Human act
61	2721	99.9	2563	2	AAK22685	Human act
62	2722	99.9	2563	2	AAK22685	Human act
63	2					

## ALIGNMENTS

RESULT 1
AAZ22692 standard; cDNA, 2563 BP.
X X AAX22685;
X X AAX22687;
X X 27-MAY-1999 (first entry)
X X Human activin receptor pre-cursor cDNA.
X X Activin receptor; activin/TGF-superfamily; receptor protein; function:
X X activity; modulate; treatment; carcinogenesis; wound healing; fertility;
X X immune system disorder; central nervous system disorder; human;
X X reproductive system; sa.
X X Homo sapiens.
X X
TH Key Location/Qualifiers
CDS /start
T /tag
T /product= "activin receptor precursor"
X X US885794-A.
X X 23-MAR-1999.
X X 02-SEP-1994; 94US-00300584.
X X 10-MAY-1991; 91US-00698709.
X X 09-OCT-1991; 91US-00773228.
X X 08-MAY-1992; 92US-00860220.
X X {SALK } SALK INST BIOLOGICAL STUDIES.
X X Vale WW, Mathews IS;
X X WPI; 1999-228514/19.
X X P-58DB; AA93211.
X X Isolated nucleic acid molecules encoding vertebrate activin receptor
X X polypeptides useful as probes for detecting similar sequences and for
X X investigating the function of the receptor in conditions such as
X X immunodeficiency, wound healing and disorders of the immune, central
X X nervous and reproductive systems.
X X Disclosure; Page: 28pp; English.



1861 CTCGAGAGATGTCGCTCCGATGACGAGCTTTTCGACCTGCTCATGAGATT 1920  
b 1861 CTCGAGAGATGTCGCTCCGATGACGAGCTTTTCGACCTGCTCATGAGATT 1920  
1921 GCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
b 1921 GCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
1921 GCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
b 1921 GCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
1981 ACTGCTATTTTTTAAATGAAAGATTTCTGATTTGATTTTAAAGAGGTAACTTT 2040  
b 1981 ACTGCTATTTTTTAAATGAAAGATTTCTGATTTGATTTTAAAGAGGTAACTTT 2040  
2041 ATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100  
b 2041 ATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100  
2101 AATGCTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
b 2101 AATGCTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
2161 ACTGCTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220  
b 2161 ACTGCTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220  
2221 TTATTAATGTAAGAACTACAGATGATTAATCAATGCTGCTGCTGCTGCTGCTGCTG 2280  
b 2221 TTATTAATGTAAGAACTACAGATGATTAATCAATGCTGCTGCTGCTGCTGCTGCTG 2280  
2281 TAATTAATGTAAGAACTACAGATGATTAATCAATGCTGCTGCTGCTGCTGCTGCTG 2340  
b 2281 TAATTAATGTAAGAACTACAGATGATTAATCAATGCTGCTGCTGCTGCTGCTGCTG 2340  
2341 TAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400  
b 2341 TAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400  
2401 AATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460  
b 2401 AATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460  
2461 AATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520  
b 2461 AATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520  
2521 CAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580  
b 2521 CAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580

RESULT 2

ACB5299  
X ACB5299 standard; cDNA, 2563 BP.  
X AAC85299;  
X AAC85299 (first entry)  
X 29-MAR-2001  
X Human activin receptor cDNA.  
X Mouse, human; rat; Xenopus; activin receptor; ligand binding domain;  
X Transmembrane domain; receptor domain; serine kinase; type beta;  
X Transforming growth factor-beta; carcinogenesis; cancer; wound healing;  
X ss.  
X Homo sapiens.  
X location/Qualifiers  
X Key  
X CDS  
X /tag= a  
X /product= "activin receptor"  
X /tag= b  
X 185..187  
X sig\_peptide  
X  
X unsure

FT /tag= c  
FT /note= "Encodes Lys"  
FT 344..346  
FT /tag= e  
FT /note= "Encodes Val"  
FT 532..534  
FT /tag= e  
FT /note= "Encodes Gln"  
X US612896-A.  
X 19-DEC-2000.  
X 07-JUN-1995;  
X 10-MAY-1993;  
X 91US-00649709.  
X 91US-00773229.  
X 09-OCT-1991;  
X 92US-00860220.  
X 08-MAY-1992;  
X 92US-00860220.  
X 02-SEP-1994;  
X 94US-00300594.  
X ISALK 1; SALK INST BIOLOGICAL STUDIES.  
X Teuchida K, Vale MW, Mathews LW;  
X P-PS05; ABM47027.  
X NPI; 2001-090408/10.  
X Novel vertebrate activin receptor having extracellular ligand binding  
X domain, transmembrane domain and intracellular serine/threonine kinase  
X domain is useful for diagnosing and treating e.g. carcinogenesis, wound  
X healing.  
X Claim 1; Page: 33pp; English.  
X This sequence encodes a human-derived activin receptor. The activin  
X extracellular, ligand binding domain, a hydrophobic, transmembrane domain  
X and an intracellular, receptor domain having serine kinase-like activity.  
X These proteins have binding affinity for at least one member of the activin  
X receptor proteins of the invention can be employed for a variety of  
X therapeutic uses, e.g. to block receptors. The presence of the soluble  
X proteins will compete with functional ligand binding, thereby blocking  
X the normal regulatory action of the complex. The receptor proteins are  
X useful for the diagnosis and therapeutic management of carcinogenesis,  
X wound healing, disorders of the immune system, reproductive system, and  
X other diseases. The sequence is not shown in the specification but is  
X derived from the mouse-derived activin receptor coding sequence (see  
X ACB5297)  
X  
X Sequence 2563 BP; 772 A; 484 C; 584 G; 720 T; 0 U; 3 other;  
Query Match 99.9%; Score 2561.2; DB 4; Length 2563;  
X  
X Residue Similarity 99.9%; P-Value 0.00; Field Size 100;  
X  
X Matches 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
X  
X  
X 1 CTCGAGAGATGTCGCTCCGATGACGAGCTTTTCGACCTGCTCATGAGATTCTTCGCG 60  
X  
X 1 CTCGAGAGATGTCGCTCCGATGACGAGCTTTTCGACCTGCTCATGAGATTCTTCGCG 60  
X  
X 61 CTCGAGAGATGTCGCTCCGATGACGAGCTTTTCGACCTGCTCATGAGATTCTTCGCG 120  
X  
X 61 CTCGAGAGATGTCGCTCCGATGACGAGCTTTTCGACCTGCTCATGAGATTCTTCGCG 120  
X  
X 121 TCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
X  
X 121 TCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
X  
X 181 GCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
X  
X 181 GCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240











DB	2521	CAAGCCAGTGAAGAAACCTTAAACACAGCTCTTACCAATATACC	2563
DB	1441	GATAGAGAGATGTTGGGATCATGAGCAGACAGAGCTTATACAGTGAATCTGTGTAGTGA	1500
DB	1501	AGAGATTAATGATATGATGAAATCAATATATGATATCTTATGAGAGATGATGATGAT	1560
DB	1501	AGAGATTAATCATCATCAAGAGCTATCAATATATATCTATCAAGAGACATATGTATGAT	1560
DB	1561	GGGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1620
DB	1561	GGGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1620
DB	1621	CGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	1680
DB	1621	CGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	1680
DB	1661	TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1740
DB	1661	TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1740
DB	1741	CTGTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1800
DB	1741	CTGTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1800
DB	1801	CAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1860
DB	1801	CAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1860
DB	1861	CTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1920
DB	1861	CTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1920
DB	1921	CGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1980
DB	1921	CGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1980
DB	1981	ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2040
DB	1981	ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2040
DB	2041	ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2100
DB	2041	ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2100
DB	2101	ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2160
DB	2101	ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2160
DB	2161	CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2220
DB	2161	CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2220
DB	2221	TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2280
DB	2221	TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2280
DB	2281	TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2340
DB	2281	TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2340
DB	2341	TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2400
DB	2341	TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2400
DB	2401	AAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2460
DB	2401	AAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2460
DB	2461	ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2520
DB	2461	ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2520
DB	2521	CAAGCCAGTGAAGAAACCTTAAACACAGCTCTTACCAATATACC	2563







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US2001:039036-A1
08-NOV-2001.
19-DEC-2000; 2600US-00742684.
10-MAY-1991; 91US-00638709.
08-MAY-1992; 92US-00860220.
08-MAY-1992; 94US-00800220.
02-SEP-1994; 92US-00100584.
07-JUN-1995; 95US-00761213.
(SALK) SALK INST BIOLOGICAL STUDIES.
Mathews LS, Vale WW, Tsuchida K,
WPI: 2002-040721/05.
P-FSD9; A0014118.
New receptor proteins having an extracellular ligand-binding domain, a
hydrophobic trans-membrane domain, and an intracellular receptor domain,
useful for diagnosing or treating carcinogenesis, wound healing or immune
disorders.
Example 11: Page 12-15; 33pp; English.
This polynucleotide sequence represents the cDNA encoding a mouse-derived
activin receptor. The invention relates to cloning and recombinant
production of receptor(s) of the activin/TGF-beta transforming growth
factor-beta superfamily. The invention identifies and characterises
distinct domains: an extracellular ligand-binding domain, a hydrophobic
trans-membrane domain, and an intracellular receptor domain having
these domains are useful in the diagnosis and therapeutic management of
carcinogenesis, wound healing, disorders of the immune, reproductive, or
central nervous systems. The receptor proteins of the invention can be
used in a variety of assays to detect the presence of activin, and as
activin-dependent targets to enhance the survival of brain neurons and
ablation in livestock and other domesticated animals, and induce twinning
in livestock and other domesticated animals. The DNAs are useful as
primers for the synthesis of complementary DNAs, and as coding sequences
protein and as coding sequences which can be used for the recombinant
expression of the receptor proteins. Agonists for TGF-beta specific
receptors can be used to stimulate wound healing, to suppress growth of
tumors, to suppress rejection of transplants, and to suppress rejection
of transplant organ). The receptor proteins of the invention
have cytostatic, vulnerary, and immunosuppressive activity.
Sequence 2563 BP; 775 A; 493 C; 585 G; 720 T; 0 U; 0 Other;
Query Match      99.7% Score 2556.4; DB 6; Length 2563;
Blast Local Similarity 99.8% Field No.0;
Matrix 2557, Conservative 2, Nucleotides 4; Indels 0; Gaps 0;
1 CTCGAGACACCGGAGATCGATGATCTACGAGAACTCTGAGCTCTCGCG 60
1 CTCGAGACACCGGAGATCGATGATCTACGAGAACTCTGAGCTCTCGCG 60
61 CTCGAGAAATGAGAGCTCTGAAAGTGGCTCTGCGCTCTTATCTCTTC 120
61 CTCGAGAAATGAGAGCTCTGAAAGTGGCTCTGCGCTCTTATCTCTTC 120
121 TTGATGCTCTATCTCGTGTCGAGAACTCGAGATCTTCTTATCTATTG 180
121 TTGATGCTCTATCTCGTGTCGAGAACTCGAGATCTTCTTATCTATTG 180
181 GGAAAGACGACGACCAACCGATGCTGTGATCTTCTTATCTGTAAGTAA 240
181 GGAAAGACGACGACCAACCGATGCTGTGATCTTCTTATCTGTAAGTAA 240

```



1321. AGAAATGGCGCAGCATCAATCTCTTACAGTATATCGAGAGGTGGTGTGCGTATAAAAAA 1380  
1322. AGAAATGGCGCAGCATCAATCTCTTACAGTATATCGAGAGGTGGTGTGCGTATAAAAAA 1381  
1381. GAGCGCTCTTGAAGGAGTATTTGGCGAGAAATGACAGAGATGCGATCTGTGTGAAAC 1440  
1382. GAGCGCTCTTGAAGGAGTATTTGGCGAGAAATGACAGAGATGCGATCTGTGTGAAAC 1441  
1383. GAGCGCTCTTGAAGGAGTATTTGGCGAGAAATGACAGAGATGCGATCTGTGTGAAAC 1440  
1441. GATAGAGAAATGTTGGAGATCATATGACAGACCAAGTTATACAGCTGGATGTGAGTGA 1500  
1442. GATAGAGAAATGTTGGAGATCATATGACAGACCAAGTTATACAGCTGGATGTGAGTGA 1501  
1501. AAGAAATCTACAGTATGAGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1560  
1502. AAGAAATCTACAGTATGAGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1561  
1503. AAGAAATCTACAGTATGAGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1560  
1561. GGTCAAGATGTTGAGAAATGATGATCTCTCTCCCAAGAGATCTAGTGTATGATGTTG 1620  
1562. GGTCAAGATGTTGAGAAATGATGATCTCTCTCCCAAGAGATCTAGTGTATGATGTTG 1621  
1621. CGGTCTACATGAGATGAGATGAGATCTGATCTGAGATGAGATGAGATGAGATGAGATG 1680  
1622. CGGTCTACATGAGATGAGATGAGATCTGATCTGAGATGAGATGAGATGAGATGAGATG 1681  
1681. TTATGTTATTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1740  
1682. TTATGTTATTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1741  
1741. CTTGTGGAAACATGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1800  
1742. CTTGTGGAAACATGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1801  
1743. CTTGTGGAAACATGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1860  
1801. CAGATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1860  
1802. CAGATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1861  
1861. CTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1920  
1921. CTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1920  
1922. CTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1980  
1981. ACTGCTATTTTATTAAGAAACATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2040  
1982. ACTGCTATTTTATTAAGAAACATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2040  
1983. ACTGCTATTTTATTAAGAAACATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2040  
2041. ATTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2100  
2042. ATTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2100  
2101. ATGTTGTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2160  
2102. ATGTTGTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2160  
2161. CTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2220  
2162. CTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2220  
2221. TTATTAATTTGAGAAACATCAAGATTTGATTAATCAATGCTCAATGTTTATTAACAGGT 2280  
2222. TTATTAATTTGAGAAACATCAAGATTTGATTAATCAATGCTCAATGTTTATTAACAGGT 2280  
2281. TAATTAAGATTAATCAATGTTTATTAAGAAACATTTGATTAATCAATGCTCAATGTTT 2340  
2282. TAATTAAGATTAATCAATGTTTATTAAGAAACATTTGATTAATCAATGCTCAATGTTT 2340  
2341. TAAGTGGCTATTGTTAAGCAGGTGTTTACGTTCTTCTACATGCGCTGTATTTATGAGA 2400  
2402. TAAGTGGCTATTGTTAAGCAGGTGTTTACGTTCTTCTACATGCGCTGTATTTATGAGA 2400  
2403. TAAGTGGCTATTGTTAAGCAGGTGTTTACGTTCTTCTACATGCGCTGTATTTATGAGA 2460  
2404. TAAGTGGCTATTGTTAAGCAGGTGTTTACGTTCTTCTACATGCGCTGTATTTATGAGA 2460

[illegible]











694 CCGAGCAGACCCCGACTCTTCCTTACTAGTGTGTGAAACGCTGCAGCTTATGAGGT 753  
761 GAAGACAGAGGAGATTTGGTGTCTGGAAAGCCCAATTTCTCAATGAATATGGC 720  
766 GAGGAGAGGAGGAGATTTGGTGTCTGGAAAGCCCAATTTCTCAATGAATATGGC 813  
771 GGTGCAATATTTCCATATCAGGACAGAGCTCTGGAGAGATGAATATGAGCTATAG 780  
814 TGTCAATATTTCCATATCAGGACAGAGCTCTGGAGAGATGAATATGAGCTATAG 873  
781 TCTACTGGATATGAGATATGAGACATCTACAGTCTATGTGTGACAGAGAAAGGAC 840  
874 TCTCTGGATATGAGATATGAGACATCTACAGTCTATGTGTGACAGAGAAAGGAC 933  
841 CAGTGTGTGTGGATCTGGCTATCATCAGAGATTTCTGAAAGGGGTCTAGTCTAGA 900  
934 CAGTGTGTGTGGATCTGGCTATCATCAGAGATTTCTGAAAGGGGTCTAGTCTAGA 993  
901 CTTTCTTAGGTCTAAATGTGTCTCTGGATCTATCTATATTCGAAAGAGAGGCG 960  
994 CTTTCTTAGGTCTAAATGTGTCTCTGGATCTATCTATATTCGAAAGAGAGGCG 1053  
961 TAGAGATTCGCTATTCATGAGATATGAGATCTGGCTATGAAAGATGCGACAGCTGC 1020  
1054 TAGAGATTCGCTATTCATGAGATATGAGATCTGGCTATGAAAGATGCGACAGCTGC 1113  
1021 AATCTCAGAGGACCTCAAAATGAAATGCTGTGTAAGAAACATCTGACAGCTG 1080  
1114 CATATTCAGAGGACCTCAAAATGAAATGCTGTGTAAGAAACATCTGACAGCTG 1173  
1081 CATCTGCTATCTGGCTGTGAGCTTAAAGTCTGAGCTGTGTAAGAAACATCTGACAGCTG 1140  
1174 CATCTGCTATCTGGCTGTGAGCTTAAAGTCTGAGCTGTGTAAGAAACATCTGACAGCTG 1233  
1141 TGGACAGCTTGTATCCCGAGAGATATGCTCTCAGAGCTGTGTGGAGGTCTATTAAGT 1200  
1234 TGGACAGCTTGTATCCCGAGAGATATGCTCTCAGAGCTGTGTGGAGGTCTATTAAGT 1293  
1201 CAAAGGACAGCTATCTGAGATATGATATGATACGCTATGAGTATGCTATGAGTAT 1260  
1294 CAAAGGACAGCTATCTGAGATATGATATGATACGCTATGAGTATGCTATGAGTAT 1353  
1261 GGTCTCTGTGATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1320  
1354 GGTCTCTGTGATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1413  
1321 AGAATTCGTGCTATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1380  
1414 GGAATTCGTGCTATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1473  
1381 GAGCTGCTATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
1474 GAGCTGCTATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1533  
1441 GAT 1500  
1534 CATGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1593  
1501 AGAATTCGTGCTATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1560  
1594 AGAATTCGTGCTATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1653  
1561 GGTCTCTGTGATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
1654 GGTCTCTGTGATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1713  
1621 GGTCTCTGTGATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
1714 CATCTGTGCTATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1773  
1681 TT--ATTGATGATCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1738  
1774 TTAGCTATTTCTCTGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833

1739 CCGTGTGAGAGCATGATCTGGAGATGATCTGGAACTCTAGCTATGCTGTGAC 1798  
1834 ACCCTTTGTGAAA-----ATGTGCTCTGGAGACTCTACTGATTCGCGAC 1893  
1799 CAGCATATGAG---AGAGGTCTAGCGGAAAGCTGCAACTGTA----AAGBACTTC 1850  
1884 GATGATGTGAGCGATGAGCTGAGCGAACTCTAGCGAACTCTATGAAAGAACTTTTG 1943  
1851 TGAATATGCTCAGAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1910  
1944 AAGAGTGTATGAGAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 2003  
1911 TCAAGTATTCAGAACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1970  
2004 TGAATGCTGCTGCT---AAATGATCTGAGATTTCTTAATGCTGAGAGCACTAACTCT 2062  
1971 TGAATGCTGCTGCT---AAATGATCTGAGATTTCTTAATGCTGAGAGCACTAACTCT 2030  
2063 TGAATGCTGCTGCT---AAATGATCTGAGATTTCTTAATGCTGAGAGCACTAACTCT 2122  
2031 GTAC---TTTTTATGATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2087  
2123 GTACCTGCTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185  
2088 GTACCTGCTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2142  
2183 GACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2242  
2146 GTTACGATGAAGAGGCTTCCAGCACTTACTTACTTCTCCCAAGCACTGACTCTGCT 2205  
2243 GTTACGATGAAGAGGCTTCCAGCACTTACTTACTTCTCCCAAGCACTGACTCTGCT 2302  
2206 TCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2265  
2303 TCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2353  
2265 GTTTTATACAGGCTTATACAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2324  
2354 AATTCATCTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2413  
2325 TGTCTAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2384  
2414 TGTCTAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2473  
2385 GTTGTGATTTAGGAGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2425  
2474 GTTGTGATTTAGGAGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2514

RESULT 2

1D AAS94867 standard; DNA; 5286 bp.  
XX AAS94867;  
AC AAS94867;  
AT AAS94867;  
GT AAS94867;  
TT AAS94867;  
XX  
14-FEB-2002 (first entry)  
Human DNA sequence #122 expressed during foam cell differentiation.  
DE Human; foam cell differentiation; atherosclerosis; cerebral stroke;  
XM cardiovascular disorder; coronary artery disease; gene therapy; ds.  
XX Homo sapiens.  
XX  
XX MO20177389-J2.  
XX  
XX 18-OCT-2001.  
XX  
XX 04-JUN-2001; 2001MO-US011128.  
XX  
XX 05-APR-2003; 2000US-0195108P.  
XX





[illegible]

## RESULT 13

ABZ35028	
ID	ABZ35028 standard; cDNA, 2382 bp.
XX	XX
XX	ABZ35028;
XX	XX
XX	05-FEB-2003 (first entry)
XX	Human gene expression profile polynucleotide SEQ ID NO 40.
XX	XX
XX	XX Human artery; endothelium; umbilical vein; aorta; pulmonary artery;
XX	XX bronchial epithelium; prostate muscle; lung fibroblast; pericardium;
XX	XX tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
XX	XX Gene expression; gene; ss.
XX	XX Homo sapiens.
XX	XX NC020274:979-142.
XX	XX
XX	26-SEP-2002.
XX	XX







2y 1850 CTGAATATGACTGAGATGCGCTCTCCAAATCAGAGATCTTTTGACTGCTA 1309  
 Db 1321 CTGAATGCTACTGAGATGCGCTCTCCAAATCAGAGATCTTTTGACTGCTA 1380  
 2y 1910 ATCAATATGCTGAAATCTGACGAGATCTTATCTCTCAGAGACTATTC 1369  
 Db 1381 ATCAATATGCTGAAATCTGACGAGATCTTATCTCTCAGAGACTATTC 1440  
 2y 1970 TTAATGACTGCTGATTTTTTTT 1995  
 Db 1441 TTAATGACTGCTGATTTTTTTT 1466

Search completed: February 26, 2004, 03:03:15  
 Job time : 940 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2004, 00:08:26 Search time 9674 Seconds

File: US-09-742-684a-15  
Patent score: 11493.171 Million call updates/sec

Sequence: 1 cccagggaagaccaggga.....aacagccttaacaatggc 2563

Scoring table: JEMMITTY\_NOC

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6400544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 04

Listing first 100

Database: GenBank

- 1: gb:ba\*
- 2: gb:ba\*
- 3: gb:ba\*
- 4: gb:ba\*
- 5: gb:ov\*
- 6: gb:ov\*
- 7: gb:ba\*
- 8: gb:ba\*
- 9: gb:ba\*
- 10: gb:ba\*
- 11: gb:ba\*
- 12: gb:ba\*
- 13: gb:un\*
- 14: gb:un\*
- 15: gb:un\*
- 16: gb:un\*
- 17: gb:un\*
- 18: gb:un\*
- 19: gb:un\*
- 20: gb:un\*
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- 33: gb:un\*
- 34: gb:un\*
- 35: gb:un\*
- 36: gb:un\*
- 37: gb:un\*
- 38: gb:un\*
- 39: gb:un\*
- 40: gb:un\*
- 41: gb:un\*
- 42: gb:un\*
- 43: gb:un\*
- 44: gb:un\*
- 45: gb:un\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result:	No.	Score	Query	Match	Length	DB	ID	Description
1	2563	4	99.7	2563	6	AR16087	Sequence	AR16087 Sequence
2	2564	4	99.7	2563	6	AR16087	Sequence	AR16087 Sequence
3	2565	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
4	2566	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
5	2567	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
6	2568	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
7	2569	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
8	2570	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
9	2571	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
10	2572	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
11	2573	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
12	2574	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
13	2575	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
14	2576	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
15	2577	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
16	2578	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
17	2579	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
18	2580	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
19	2581	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
20	2582	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
21	2583	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
22	2584	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
23	2585	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
24	2586	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
25	2587	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
26	2588	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
27	2589	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
28	2590	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
29	2591	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
30	2592	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
31	2593	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
32	2594	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
33	2595	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
34	2596	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
35	2597	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
36	2598	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
37	2599	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
38	2600	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
39	2601	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
40	2602	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
41	2603	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
42	2604	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
43	2605	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
44	2606	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ
45	2607	4	99.7	2563	6	MUSACTR	Mus musculus	M45287 Mouse activ

ALIGNMENTS

RESULT 1	LOCUS	ARL16087	Sequence 12 from patent US 6132988	DNA	linear	PAT 16-MAY-2001
1	LOCUS	ARL16087	Sequence 12 from patent US 6132988	DNA	linear	PAT 16-MAY-2001
2	DEFINITION	ARL16087	Sequence 12 from patent US 6132988	DNA	linear	PAT 16-MAY-2001
3	ACCESSION	ARL16087	Sequence 12 from patent US 6132988	DNA	linear	PAT 16-MAY-2001
4	KEYWORDS	ARL16087.1	GI:14096409	DNA	linear	PAT 16-MAY-2001
5	ORGANISM	Unknown.		DNA	linear	PAT 16-MAY-2001
6	REFERENCE	1 (bases 1 to 2563)		DNA	linear	PAT 16-MAY-2001
7	TITLE	Sugino H., Nakamura T. and Shouji H.		DNA	linear	PAT 16-MAY-2001
8	AUTHORS	DNA encoding a neuronal cell-specific receptor protein		DNA	linear	PAT 16-MAY-2001
9	FEATURES	Patent: US 6132988		DNA	linear	PAT 16-MAY-2001
10	FEATURES	Location/Qualifiers		DNA	linear	PAT 16-MAY-2001

Prod. No. is the number of results predicted by chance to have a

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Search completed: February 26, 2004, 05:45:04  
Job time : 9995 secs